SUBSTITUTE SEQUENCE LISTING

<110> RIKEN
KABUSHIKI KAISHA DNAFORM

<120> Method for utilizing the 5'end of mRNA for cloning and analysis

<130> 1336(PCT) [035576/285978]

<140> US 10/517,544
<141> 2005-06-09

<150> JP 2002-171851
<151> 2002-06-12

<150> JP 2002-235294
<151> 2002-08-12

<160> 119

<170> PatentIn version 3.1

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<223> Primer 1 (uni-PCR)

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<400> 24
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<400> 26
caggaaacag ctatgac 17

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cggacctaga gtttttcgta tgtttgtcat cgtcggacct aggtccgacg gtccattcct 180
gagagtctct ctaggtccga cgagagagag aggatccttc tgtctagacc ctgacgccgg 240
aaccgcaccg tcggacctag gtccgacgga aaagcagctt cctccactct aggtccgacg 300
gtgtgtgtgt gtgtgcgtgt tctagagact ggttcagatc aaaagtcgtc ggacctaggt 360
ccgacggggc tggtgagatg gctcagtcta gatgcatgct cgagcggccg ccagtgtgat 420
ggatatctgc cnaatnccag cacaccggcg cgcgcnacca gtggatccga gcccggtacc 480
aagcttgatg catacctcga gtatcctata ctgtcaccta aatagcttgg ggtaatcatg 540
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ngttggacct aggtccaacn 20

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c atg ccg ccc tcc ggg ctg cgg ctg ctg ccg ctg ctg cta ccg ctg ctg 889
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tgg cta ctg gtg ctg acg cct ggc ccg ccg gcc gcg gga cta tcc acc 937
Trp Leu Leu Val Leu Thr Pro Gly Pro Pro Ala Ala Gly Leu Ser Thr
            20   25   30
tgc aag act atc gac atg gag ctg gtg aag cgg aag cgc atc gag gcc 985
Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
        35   40   45
atc cgc ggc cag atc ctg tcc aag ctg cgg ctc gcc agc ccc ccg agc 1033
Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
    50   55   60
cag ggg gag gtg ccg ccc ggc ccg ctg ccc gag gcc gtg ctc gcc ctg 1081
Gln Gly Glu Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65   70   75   80
tac aac agc acc cgc gac cgg gtg gcc ggg gag agt gca gaa ccg gag 1129
Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Ala Glu Pro Glu
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ccc gag cct gag gcc gac tac tac gcc aag gag gtc acc cgc gtg cta 1177
Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
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atg gtg gaa acc cac aac gaa atc tat gac aag ttc aag cag agt aca 1225
Met Val Glu Thr His Asn Glu Ile Tyr Asp Lys Phe Lys Gln Ser Thr
        115   120   125
cac agc ata tat atg ttc ttc aac aca tca gag ctc cga gaa gcg gta 1273
His Ser Ile Tyr Met Phe Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
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cct gaa ccc gtg ttg ctc tcc cgg gca gag ctg cgt ctg ctg agg agg 1321
Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Arg
145   150   155   160
ctc aag tta aaa gtg gag cag cac gtg gag ctg tac cag aaa tac agc 1369
Leu Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser
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aac aat tcc tgg cga tac ctc agc aac cgg ctg ctg gca ccc agc gac 1417
Asn Asn Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp
            180   185   190
tcg cca gag tgg tta tct ttt gat gtc acc gga gtt gtg cgg cag tgg 1465
Ser Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp
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ttg agc cgt gga ggg gaa att gag ggc ttt cgc ctt agc gcc cac tgc 1513
Leu Ser Arg Gly Gly Glu Ile Glu Gly Phe Arg Leu Ser Ala His Cys
    210   215   220

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Ser Cys Asp Ser Arg Asp Asn Thr Leu Gln Val Asp Ile Asn Gly Phe
225                 230                 235                 240
act acc ggc cgc cga ggt gac ctg gcc acc att cat ggc atg aac cgg     1609
Thr Thr Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg
                245                 250                 255
cct ttc ctg ctt ctc atg gcc acc ccg ctg gag agg gcc cag cat ctg     1657
Pro Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu
            260                 265                 270
caa agc tcc cgg cac cgc cga gcc ctg gac acc aac tat tgc ttc agc     1705
Gln Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Tyr Cys Phe Ser
        275                 280                 285
tcc acg gag aag aac tgc tgc gtg cgg cag ctg tac att gac ttc cgc     1753
Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg
    290                 295                 300
aag gac ctc ggc tgg aag tgg atc cac gag ccc aag ggc tac cat gcc     1801
Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala
305                 310                 315                 320
aac ttc tgc ctc ggg ccc tgc ccc tac att tgg agc ctg gac acg cag     1849
Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln
                325                 330                 335
tac agc aag gtc ctg gcc ctg tac aac cag cat aac ccg ggc gcc tcg     1897
Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser
            340                 345                 350
gcg gcg ccg tgc tgc gtg ccg cag gcg ctg gag ccg ctg ccc atc gtg     1945
Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val
        355                 360                 365
tac tac gtg ggc cgc aag ccc aag gtg gag cag ctg tcc aac atg atc     1993
Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile
    370                 375                 380
gtg cgc tcc tgc aag tgc agc tga ggtcccgccc cgccccgccc cgccccggca    2047
Val Arg Ser Cys Lys Cys Ser
385                 390
ggcccggccc caccccgccc cgcccccgct gccttgccca tgggggctgt atttaaggac   2107
accgtgcccc aagcccacct ggggccccat taaagatgga gagaggactg cggatctctg   2167
tgtcattggg cgcctgcctg gggtctccat ccctgacgtt cccccactcc cactccctct   2227
ctctccctct ctgcctcctc ctgcctgtct gcactattcc tttgcccggc atcaaggcac   2287
aggggaccag tggggaacac tactgtagtt agatctattt attgagcacc ttgggcactg   2347
ttgaagtgcc ttacattaat gaactcattc agtcaccata gcaacactct gagatggcag   2407
ggactctgat aacacccatt ttaaaggttg aggaaacaag cccagagagg ttaagggagg   2467
agttcctgcc caccaggaac ctgctttagt gggggatagt gaagaagaca ataaaagata   2527
gtagttcagg ccaggcgggg tgctcacgcc tgtaatccta gcacttttgg gaggcagaga   2587
tgggaggata cttgaatcca ggcatttgag accagcctgg gtaacatagt gagaccctat   2647
ctctacaaaa cacttttaaa aaatgtacac ctgtggtccc agctactctg gaggctaagg   2707
tgggaggatc acttgatcct gggaggtcaa ggctgcag                           2745
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<210> 77
<211> 391
<212> PRT
<213> Homo sapiens

<400> 77

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Met Pro Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
1               5                   10                  15
Trp Leu Leu Val Leu Thr Pro Gly Pro Pro Ala Ala Gly Leu Ser Thr
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```
            20                  25                  30

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
        35                  40                  45
Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
    50                  55                  60
Gln Gly Glu Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65                  70                  75                  80
Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Ala Glu Pro Glu
                85                  90                  95
Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
            100                 105                 110
Met Val Glu Thr His Asn Glu Ile Tyr Asp Lys Phe Lys Gln Ser Thr
        115                 120                 125
His Ser Ile Tyr Met Phe Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
    130                 135                 140
Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Arg
145                 150                 155                 160
Leu Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser
                165                 170                 175
Asn Asn Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp
            180                 185                 190
Ser Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp
        195                 200                 205
Leu Ser Arg Gly Gly Glu Ile Glu Gly Phe Arg Leu Ser Ala His Cys
    210                 215                 220
Ser Cys Asp Ser Arg Asp Asn Thr Leu Gln Val Asp Ile Asn Gly Phe
225                 230                 235                 240
Thr Thr Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg
                245                 250                 255
Pro Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu
            260                 265                 270
Gln Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Tyr Cys Phe Ser
        275                 280                 285
Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg
    290                 295                 300
Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala
305                 310                 315                 320
Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln
                325                 330                 335
Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser
            340                 345                 350
Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val
        355                 360                 365
Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile
    370                 375                 380
Val Arg Ser Cys Lys Cys Ser
385                 390
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<210> 78
<211> 596
<212> DNA
<213> Artificial Sequence

<220>

<223> pZeRO-1 vector with masked portions

<220>
<221> misc_feature
<222> (1)...(596)
<223> "n" = any nucleotide

<400> 78
tcgttannnn nnnnnnnnnn nnnnnnnnnn nngtcgacga gttctcagca gagccgccgt 60
ctagagcccc gccctcccgg gccaccgtcg gacctagaat agttactcga ggtctctcgt 120
cggacctaga gtttttcgta tgtttgtcat cgtcggacct aggtccgacg gtccattcct 180
gagagtctct ctaggtccga cgagagagag aggatccttc tgtctagacc ctgacgccgg 240
aaccgcaccg tcggacctag gtccgacgga aaagcagctt cctccactct aggtccgacg 300
gtgtgtgtgt gtgtgcgtgt tctagagact ggttcagatc aaaagtcgtc ggacctaggt 360
ccgacggggc tggtgagatg gctcagnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 420
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 480
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 540
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnng 596

<210> 79
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Linker

<400> 79
tctaggtccg acg 13

<210> 80
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Linker

<400> 80
cctaggtccg acg 13

<210> 81
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Linker

<400> 81
tctaggtccg acg 13

<210> 82

<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Linker

<400> 82
cctaggtccg acg 13

<210> 83
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Linker

<400> 83
cctaggtccg acg 13

<210> 84
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Linker

<400> 84
tctaggtccg acg 13

<210> 85
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Linker

<400> 85
cctaggtccg acg 13

<210> 86
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Linker

<400> 86
cctaggtccg acg 13

<210> 87
<211> 597
<212> DNA
<213> Artificial Sequence

<220>
<223> zzb21305i03t3 masked vector

<220>
<221> misc_feature
<222> (1)...(597)
<223> n = any nucleotide

<400> 87
tcgttannnn nnnnnnnnnn nnnnnnnnnn nngtcgacga gttctcagca gagccgccgt 60
ctagagcccc gccctcccgg gccacnnnnn nnnnnnnnat agttactcga ggtctctnnn 120
nnnnnnnnng ttttttcgtat gtttgtcatn nnnnnnnnnn nnnnnnnnng tccattcctg 180
agagtctcnn nnnnnnnnnn nagagagaga ggatccttct gtctagacct gacgccggaa 240
ccgcacnnnn nnnnnnnnnn nnnnnngaaa agcagcttcc tcctccacnn nnnnnnnnnn 300
ngtgtgtgtg tgtgtgcgtg ttctagagac tggttcagat caaaagtnnn nnnnnnnnnn 360
nnnnnnnggg ctggtgagat ggctcagnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 420
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 480
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 540
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnng   597

<210> 88
<211> 596
<212> DNA
<213> Artificial Sequence

<220>
<223> zzb21305i03t3 vector

<220>
<221> misc_feature
<222> (1)...(596)
<223> n = any nucleotide

<400> 88
tcgttannnn nnnnnnnnnn nnnnnnnnnn nngtcgacga gttctcagca gagccgccgn 60
nnnnngcccc gccctcccgg gccacnnnnn nnnnnnnnat agttactcga ggtctctnnn 120
nnnnnnnnng ttttttcgtat gtttgtcatn nnnnnnnnnn nnnnnnnnng tccattcctg 180
agagagtctc nnnnnnnnnn nnnagagaga gaggatcctc tgtctagacc tgacgccgga 240
accgccacnn nnnnnnnnnn nnnnnnnnga aaagcagctt cctccacnnn nnnnnnnnnn 300
gtgtgtgtgt gtgtgcgtgt tctagagact ggttcagatc aaaagtnnnn nnnnnnnnnn 360
nnnnnngggc tggtgagatg gctcagnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 420
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 480
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 540
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnng   596

<210> 89
<211> 569
<212> DNA

<213> Artificial Sequence

<220>
<223> zzb21106I09T3.scf vector

<220>
<221> misc_feature
<222> (1)...(569)
<223> n = any nucleotide

<400> 89
cattagggga ttgggcccnn nnnnnnnnnn ngtacctcct cgcatcccgc nnnnnnacct 60
tcgacacgca caccacnnnn nnnnnnnnnn nnnnnnatgg accgagggcc ccagccnnnn 120
nnnnnnnnnc ggatcgggtg ggtcggacnn nnnnacgaac tgctgcgacc tctnnnnnnn 180
nnnnnncaca gcgccggctc cggagannnn nnnnnnnnnc tcggagcctg caaagtctnn 240
nnnnnnnnnn ntccggcgct gcggcagctc cnnnnnnnnn nnnngcgacc aggtccgacg 300
gtgtnnnnnn nnnnnnngac tctgggcgag aacgtctnnn nnnnnnnnnn nnnnnnngcc 360
gttccttgct tgctggannn nnnctgagct aaatccccaa cccnnnnnnn nnnnnnnnnn 420
nnngagtaac tataacggtc ctnnnnnngc gagctccagg cggaatcnnn nnnnnnnnnn 480
acccgggggg cgggactaac cgtcggacnn nnnnnnnnnn nagggaccgc tgcggtccgn 540
nnnnnnnnnn nnnnnnnnnn nnnnnnnnn 569

<210> 90
<211> 607
<212> DNA
<213> Artificial Sequence

<220>
<223> zzc20401c11t3 masked vector

<220>
<221> misc_feature
<222> (1)...(607)
<223> n = any nucleotide

<400> 90
tgataaggca atggcctcta atgctgnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 60
nngccgccgc gccttccgcg tcnnnnnnnn nnnnnnnnnn nngagggccg ccgcccgccc 120
tccnnnnnna gttttttttt ttttttgnn nnnnnnnnnn nnnnnnnngg gcagagcgag 180
cagagcctnn nnnngtctgt cagaatcaga agtnnnnnnn nnnnnnnnnn nnngctttgc 240
agacgccact gtnnnnnnaa agtccacctg gactttccnn nnnnnnnnnn nnnnnnnncc 300
tgcgcggcct cggcggcnnn nnnaactctg ttatacacta acnnnnnnnn nnnnnnnnnn 360
nnagagactg aacagcgggc gannnnnnca gccatcttgc cccacctnnn nnnnnnnnnn 420
nnnnnnngct tgccttctgg ccatgccnnn nnnccccccc ctatgcgtgc gtcnnnnnnn 480
nnnnnnnnnn nnnagtgtgg ctgttccatg gnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 540
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 600
nnnnnng 607

<210> 91
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Tag sequence

<400> 91
acctccctcc gcggag 16

<210> 92
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Tag sequence

<400> 92
gtggtgtgcg tgtcgaaggt 20

<210> 93
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Tag sequence

<400> 93
gacgcggaag gcgcggcggc 20

<210> 94
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary elongation strand

<220>
<221> misc_feature
<222> (1)...(60)
<223> n = any nucleotide

<400> 94
agagagagac ctcgagtaac tataacggtc ctaaggtagc gacctaggtc cgacnnnnnn 60

<210> 95
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary Ist strand cDNA

<400> 95
tctctctctg gagctcattg atattgccag gattccatcg ctggatccag cgtg 54

<210> 96
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary elongation strand

<220>
<221> misc_feature
<222> (1)...(48)
<223> n = any nucleotide

<400> 96
agagagagaa ctaggcttct taataggtga agatctggag gnnnnnnn 48

<210> 97
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary 1st cDNA strand

<400> 97
tctctatctt gatccgaaga attatccact tctagacctc 40

<210> 98
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary elongation strand

<220>
<221> misc_feature
<222> (1)...(51)
<223> n = any nucleotide

<400> 98
agagagagaa ctaggcttct taataggtga ggcgcgcctg gaggnnnnnn n 51

<210> 99
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary 1st cDNA strand

<400> 99
tctctatctt gatccgaaga attatccact ccgcgcggac ctc 43

<210> 100
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary elongation strand

<220>
<221> misc_feature
<222> (1)...(49)
<223> n = any nucleotide

<400> 100
agagagagag cttagatgag agtgactcga gcctaggtcc aacgnnnnn 49

<210> 101
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary 1st cDNA strand

<400> 101
tctctctctc gaatctactc tcactgagct cggatccagg ttg 43

<210> 102
<211> 77
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary elongation strand

<220>
<221> misc_feature
<222> (1)...(77)
<223> n = any nucleotide

<400> 102
cctaggtccg acnnnnnnnn nnnnnnnnnn nntctagatc aggactcttc tatagtgtca 60
cctaaagtct ctctctc 77

<210> 103
<211> 79
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary 1st cDNA strand

<220>
<221> misc_feature
<222> (1)...(79)
<223> n = any nucleotide

<400> 103
ggatccaggc tgnnnnnnnn nnnnnnnnnn nnnnagatct agtcctgaga agatatcaca 60
gtggatttca gagagagag 79

<210> 104
<211> 71
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary elongation strand

<220>
<221> misc_feature
<222> (1)...(71)
<223> n = any nucleotide

<400> 104
agatctggag nnnnnnnnnn nnnnnngaat tctcaggact attctatagt gtcacctaaa 60
gtctctctct c 71

<210> 105
<211> 73
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary 1st cDNA strand

<220>
<221> misc_feature
<222> (1)...(73)
<223> n = any nucleotide

<400> 105
tctagacctc nnnnnnnnnn nnnnnnnnct taagagtcct gagaagatat cacagtggat 60
ttcagagaga gag 73

<210> 106
<211> 73
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary elongation strand

<220>
<221> misc_feature
<222> (1)...(73)

<223> n = any nucleotide

<400> 106
gcgcgcctgg agnnnnnnnn nnnnnnnnga attctcagga ctattctata gtgtcaccta 60
aagtctctct ctc 73

<210> 107
<211> 76
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary 1st cDNA strand

<220>
<221> misc_feature
<222> (1)...(76)
<223> n = any nucleotide

<400> 107
ccgcgcggac ctannnnnnn nnnnnnnnnn ncttaagagt cctgagaaga tatcacagtg 60
gatttcagag agagag 76

<210> 108
<211> 74
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary elongation strand

<220>
<221> misc_feature
<222> (1)...(74)
<223> n = any nucleotide

<400> 108
cctaggtcca acnnnnnnnn nnnnnnnnnn nngaattcta cgcctctcga tcgaaatccc 60
gatctaggct agcg 74

<210> 109
<211> 74
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary 1st cDNA strand

<220>
<221> misc_feature
<222> (1)...(74)
<223> n = any nucleotide

<400> 109

ggatccaggt tgnnnnnnnn nnnnnnnnnn nncttaagat gcggagagcg tgaatcgagt 60
ttaaggctag catc 74

<210> 110
<211> 68
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA fragment for concatemer production

<220>
<221> misc_feature
<222> (1)...(68)
<223> n = any nucleotide

<400> 110
tctagannnn nnnnnnnnnn nnnnngtcgg acctaggtcc gacnnnnnnn nnnnnnnnnn 60
nntctaga 68

<210> 111
<211> 68
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA fragment for concatemer production

<220>
<221> misc_feature
<222> (1)...(68)
<223> n = any nucleotide

<400> 111
agatctnnnn nnnnnnnnnn nnnnncagcc tggatccagg ctgnnnnnnn nnnnnnnnnn 60
nnagatct 68

<210> 112
<211> 68
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA fragment for concatemer production

<220>
<221> misc_feature
<222> (1)...(68)
<223> n = any nucleotide

<400> 112
tctagannnn nnnnnnnnnn nnnnngtcgg acctagannn nnnnnnnnnn nnnnnngtcg 60
gacctaga 68

<210> 113
<211> 68
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA fragment for concatemer production

<220>
<221> misc_feature
<222> (1)...(68)
<223> n = any nucleotide

<400> 113
agatctnnnn nnnnnnnnnn nnnnncagcc tggatctnnn nnnnnnnnnn nnnnnncagc 60
ctggatct 68

<210> 114
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA fragment for concatemer production

<220>
<221> misc_feature
<222> (1)...(57)
<223> n = any nucleotide

<400> 114
gaattcnnnn nnnnnnnnnn nnctccagat ctggagnnnn nnnnnnnnnn ngaattc 57

<210> 115
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA fragment for concatemer production

<220>
<221> misc_feature
<222> (1)...(57)
<223> n = any nucleotide

<400> 115
cttaagnnnn nnnnnnnnnn nngaggtcta gacctcnnnn nnnnnnnnnn ncttaag 57

<210> 116
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA fragment for concatemer production

<220>
<221> misc_feature
<222> (1)...(63)
<223> n = any nucleotide

<400> 116
gaattcnnnn nnnnnnnnnn nncctccagg cgcgcctgga ggnnnnnnnn nnnnnnngaa 60
ttc 63

<210> 117
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA fragment for concatemer production

<220>
<221> misc_feature
<222> (1)...(63)
<223> n = any nucleotide

<400> 117
cttaagnnnn nnnnnnnnnn nnggaggtcc gcgcggacct ccnnnnnnnn nnnnnnnctt 60
aag 63

<210> 118
<211> 68
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA fragment for concatemer production

<220>
<221> misc_feature
<222> (1)...(68)
<223> n = any nucleotide

<400> 118
gaattcnnnn nnnnnnnnnn nnnnngttgg acctaggtcc aacnnnnnnn nnnnnnnnnn 60
nngaattc 68

<210> 119
<211> 68
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA fragment for concatemer production

<220>
<221> misc_feature
<222> (1)...(68)
<223> n = any nucleotide

<400> 119
cttaagnnnn nnnnnnnnnn nnnnncaacc tggatccagg ttgnnnnnnn nnnnnnnnnn 60
nncttaag 68